

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 16:39:25 ; Search time 231.5 Seconds
(without alignments)
14834.978 Million cell updates/sec

Title: US-10-025-514-15
Perfect score: 1525
Sequence: 1 tctagaccatgaagacccct.....ccagtcaggccctagtcgac 1525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1525	100.0	1525	ABK88025	DNA sequence encod
2	1197.4	78.5	1582	ABK88027	DNA sequence encod
3	1197.4	78.5	1756	ABK88026	DNA sequence encod
4	1191.6	78.1	1525	ABK88022	DNA sequence encod
5	1188.8	78.0	1756	ABK88023	DNA sequence encod
6	1187	77.8	1582	ABK88024	DNA sequence encod
7	1182	77.5	1182	ABK88015	DNA encoding human
8	628.4	41.2	1260	AAV41730	Codon-optimised RA
9	432.2	28.3	1312	AAQ89254	Human alpha-1-try

10	432.2	28.3	1312	19	AAV28471	Nucleotide sequenc
11	432.2	28.3	1312	21	AAZ90199	Human alpha-anti
12	429.2	28.1	1367	22	AA345052	cDNA encoding nove
13	429	28.1	1185	19	AAV41726	Native coding sequ
14	429	28.1	1352	13	AAQ31403	Human alpha-1 anti
15	429	28.1	1352	24	ABL67511	Thyroid cancer rel
16	429	28.1	1371	24	ABR84495	Human cDNA differe
17	429	28.1	1371	24	ABL67510	Thyroid cancer rel
18	429	28.1	1433	10	AAAN1077	Sequence encoding
19	429	28.1	1434	5	AAAN40078	Sequence encoding
20	429	28.1	1434	20	AAAX83548	Human alpha1-anti
21	429	28.1	5932	21	AAZ45928	Nucleotide sequenc
22	429	28.1	6142	21	AAZ45932	Nucleotide sequenc
23	429	28.1	6142	21	AAZ45933	Nucleotide sequenc
24	429	28.1	6565	21	AAZ45925	Nucleotide sequenc
25	429	28.1	6714	21	AAZ45930	Nucleotide sequenc
26	429	28.1	6924	21	AAZ45934	Nucleotide sequenc
27	429	28.1	6924	21	AAZ45935	Nucleotide sequenc
28	429	28.1	6981	21	AAZ45931	Nucleotide sequenc
29	429	28.1	7054	21	AAZ45927	Nucleotide sequenc
30	428.6	28.1	7405	21	AAZ45926	Nucleotide sequenc
31	427.6	28.0	1189	13	AAQ21125	Alpha-1-antitrypsi
32	427.4	28.0	1352	18	AAQ72858	Human alpha-1-anti
33	425.8	27.9	1312	10	AAAN97127	Sequence of alpha-
34	425.8	27.9	1434	10	AAAN90341	Sequence of alpha-
35	425.4	27.9	1185	7	AAAG0417	Human alpha 1-anti
36	424.2	27.8	1378	13	AAQ23746	Alpha-1 antitrypsi
37	424.2	27.8	1396	11	AAQ03184	Entire sequence of
38	422.6	27.7	1423	6	AAAN50425	Sequence encoding
39	421	27.6	1299	6	AAAN50540	Sequence of human
40	421	27.6	1378	6	AAAN50021	Sequence of human
41	407	26.7	1390	22	AAH23089	Osteoarthritis tis
42	402.6	26.4	2013	24	ABL59152	Sequence of fusion
43	372.6	24.4	1242	18	AAAT79493	Protease inhibitor
44	359.8	23.6	1242	18	AAAT78180	Recombinant squirr
45	357	23.4	1312	10	AAAN91078	Alpha-1-antitrypsi

ALIGNMENTS

RESULT 1

ABK88025
ID ABK88025 standard; DNA; 1525 BP.

XX AC ABK88025;

XX DT 07-OCT-2002 (first entry)

XX DE DNA sequence encoding rSLAP1 fusion protein.

XX DE rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;

XX KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;

XX KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;

XX KW human immunodeficiency virus; atopical dermatitis; muscular dystrophy;

XX KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;

XX KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;

XX KW glomerulonephritis; hypertension.

OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

FT RBS 6..8

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FT FT /standard_name= "Ribosome binding site"

FT FT 9..1520

FT FT /tag= b

FT FT /product= "rSLAP1 fusion protein"

FT FT 12..1193

FT FT /tag= c

FT FT /note= "AAT coding region"

FT FT 1194..1196

FT misc_feature /*tag= d
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FT /*tag= e
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XX WO200250287-A2.

XX PD 27-JUN-2002.

XX PF 18-DEC-2001; 2001WO-US49256.

XX PR 18-DEC-2000; 2000US-256699P.

XX PR 20-NOV-2001; 2001US-331968P.

XX PA (ARRI-) ARRIVA PHARM INC.

XX PI Barr PJ, Gibson HL, Pemberton P;

XX DR WPI; 2002-500631/53.

XX DR P-PSDB; AAU99884.

XX Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

XX Example 3; Page 89-90; 134pp; English.

XX This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha 1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rSLAP1 fusion protein of the invention.

XX Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 other;

Query Match 100.0%; Score 1525; DB 24; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCTAGACCATGAAGACCTCTAAGCGGACGCGCTCAAAAACCGACACCATCATCAG 60
QY 61 ACCAAGACCATCGACTTTTAAATAAAATTAACCCAAATTTAGCCGAATTTGCTTTTCTT 120
DB 61 ACCAAGACCATCGACTTTTAAATAAAATTAACCCAAATTTAGCCGAATTTGCTTTTCTT 120
QY 121 TGTATAGACAATAGCTCATCAAGTAATCTTCTAACAATTTTTTTAGTCTCTGTTCTTA 180
DB 121 TGTATAGACAATAGCTCATCAAGTAATCTTCTAACAATTTTTTTAGTCTCTGTTCTTA 180
QY 181 TTGCCACTGCTTCGCCATGTTAGTTAGTACTAAAGCCGATACCCATGACGAGATTT 240
DB 181 TTGCCACTGCTTCGCCATGTTAGTTAGTACTAAAGCCGATACCCATGACGAGATTT 240
QY 241 TAGAAGGTTTAACTTAATTTGACCGGAATCCAGAGACCCCAATTCACGAGGTTTTC 300
DB 241 TAGAAGGTTTAACTTAATTTGACCGGAATCCAGAGACCCCAATTCACGAGGTTTTC 300

DB 241 TAGAAGGTTTAACTTTAAATTTGACCGAAATCCAGAGACCCCAATTCACGAGGTTTTC 300
QY 301 AAGAGTTGTTGAGAACTTTGAATCAACCTGATTTCTCAATTTGCAATTAATCTACTGTTAAG 360
DB 301 AAGAGTTGTTGAGAACTTTGAATCAACCTGATTTCTCAATTTGCAATTAATCTACTGTTAAG 360
QY 361 GTTTATTTTGTCTGAAGGTTTAAAAATGTTGACAAATTCCTAGAAAGACGTTCAAGAAAC 420
DB 361 GTTTATTTTGTCTGAAGGTTTAAAAATGTTGACAAATTCCTAGAAAGACGTTCAAGAAAC 420
QY 421 TATATCATAGTAGAGGCTTTTACCGTTTAAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAA 480
DB 421 TATATCATAGTAGAGGCTTTTACCGTTTAAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAA 480
QY 481 TTAATGATTTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAG 540
DB 481 TTAATGATTTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAG 540
QY 541 ATCGTGATACCGCTTTCGCACTAGTTTAACTATATTTTTTCAAGGTAAGTGGGAACGTC 600
DB 541 ATCGTGATACCGCTTTCGCACTAGTTTAACTATATTTTTTCAAGGTAAGTGGGAACGTC 600
QY 601 CTTTCGAGGTTTAAAGTACTGAGAGAGAGATTTTTCATGTTGATCAAGTTACTACTGTCTCA 660
DB 601 CTTTCGAGGTTTAAAGTACTGAGAGAGAGATTTTTCATGTTGATCAAGTTACTACTGTCTCA 660
QY 661 AAGTCCCAATGATGAAAGACTGGGTATGTTCAATATTCACCAATTCGCAAAATTAAGTT 720
DB 661 AAGTCCCAATGATGAAAGACTGGGTATGTTCAATATTCACCAATTCGCAAAATTAAGTT 720
QY 721 CTTGGGCTTTTAAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAAGAG 780
DB 721 CTTGGGCTTTTAAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAAGAG 780
QY 781 AAGTAAAGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTTACTTAAATTTTAG 840
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QY 841 AGAACGAGGATCGTCGTCGTCGCTCTCTGCACTGCGCAAGTTTAAAGTATCACCGGTACTT 900
DB 841 AGAACGAGGATCGTCGTCGTCGCTCTCTGCACTGCGCAAGTTTAAAGTATCACCGGTACTT 900
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DB 1021 TCTTAACCTATTGATGAAAAGGTTACCGAGCGCGCGCGCTATGTTCTCTGGAAGCTATTTC 1080
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RESULT 4
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ID ABK88022 standard; DNA; 1525 BP.
AC
AC ABK88022;
XX
XX 07-OCT-2002 (first entry)
XX
XX DNA sequence encoding SLAP1 fusion protein.
XX
XX Yeast; alpha factor; gene; ds; Alzheimer's disease; SLAP1;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
```

```
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; hypertension.
XX
OS Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
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FT 9..1520
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FT /product= "SLAP1 fusion protein"
FT 12..332
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FT /note= "SLP1 coding region"
FT 333-335
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XX WO200250287-A2.
XX 27-JUN-2002.
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XX 18-DEC-2001; 2001WO-US49256.
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XX 18-DEC-2000; 2000US-256699P.
XX 20-NOV-2001; 2001US-331966P.
XX
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI: 2002-500631/53.
XX P-PSDB; RAU99881.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor.
XX
XX Example 1; Page 73-73; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active protein. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, in inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis. Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the DNA encoding the
XX SLAP1 fusion protein of the invention.
XX
XX Sequence 1525 BP; 467 A; 286 C; 314 G; 458 T; 0 other;
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XX Query Match 78.18; Score 1191.6; DB 24; Length 1525;
XX Best Local Similarity 99.7%; Pred. No. 1.6e-289;
XX Matches 1194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy	847	AGGATCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTTACGACT	906
Db	1402	AGGATCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTTACGACT	1461
Qy	907	TAAAACTGTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGGTGGCGATTTGA	966
Db	1462	TAAATCTGTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGGTGGCGATTTGA	1521
Qy	967	GTGGTGTGTTACTGAAGAAGCTCCATTAAAATTCAGTAAAGCTGTTTCACAAAGCCGCTCTTAA	1026

DB 1522 GTGGTGTTACTGAAGAAGCTCCATTAAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAA 1581

Qy 1027 CTATTGATGAAAGGGTACCGAGGCGCGCGGTATGTTCTGGAAGCTATTCCAATGA 1080
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Db 1582 CTATTGATGAAAGGGTACCGAGGCGCGCGGTATGTTCTGGAAGCTATTCCAATGA 1641

Db	1642	GCATTCCACCAGAAGTTAAATTTAATAAACCAATTGTTTTCTGATGATCGAGCAGAACA	1701
Qy	1147	CTAAAGCCCATGTTTATGGGTAAGTTGTCAACCCCAACTCAGAAGATGTC	1198
Db	1702	CTAAAGCCCATGTTTATGGGTAAGTTGTCAACCCCAACTCAGAAGTAGTC	1753
RESULT	6		
ABK88024	ID	ABK88024 standard; DNA; 1582 BP.	
XX	AC	ABK88024;	
XX	XX	07-OCT-2002 (first entry)	
XX	XX	DNA sequence encoding N-TAP1 fusion protein.	
XX	XX	NTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;	
KW	KW	malaria; emphysema; asthma; chronic obstructive pulmonary disease;	
KW	KW	cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;	
KW	KW	human immunodeficiency virus; atopic dermatitis; muscular dystrophy;	
KW	KW	herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;	
KW	KW	tumour metastasis; osteoporosis; Paget's disease; scleroderma;	
KW	KW	glomerulonephritis; hypertension.	
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OS	OS	Synthetic.	
XX	XX		
XX	XX		
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PR 18-DEC-2000; 2000US-256699P.
PR 20-NOV-2001; 2001US-331966P.
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XX
PA (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI; 2002-500631/53.
DR P-PSDB; AAU99883.
DR
XX Novel fusion protein useful for inhibiting protease activity associated
PT with a disorder such as emphysema, asthma, comprises a first protease
PT inhibitor comprising alpha 1-antitrypsin and a second protease
PT inhibitor.
XX
XX Example 2; Page 85-86; 134pp; English.
PS
XX This invention relates to a novel fusion protein comprising a first
CC protease inhibitor comprising an alpha-1-antitrypsin or its functionally
CC active portion and a second protease inhibitor or its functionally
CC active protein. The fusion proteins of the invention may act as an
CC inhibitor of protease activity. The fusion protein of the invention
CC is useful for inhibiting protease activity associated with a disorder
CC such as emphysema, asthma, chronic obstructive pulmonary disease,
CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
CC for treating an individual suffering from or at risk for a disease or
CC disorder involving unwanted protease activity. The proteins are useful
CC for treating dermatological diseases such as atopic dermatitis, eczema
CC and psoriasis, in inflammatory responses to viral infection, and for
CC treating herpes infection, corneal or epidermal ulceration, chronic
CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
CC tumour metastasis and tumour angiogenesis, gastric ulceration,
CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
CC bacterial infection, Alzheimer's disease, hypertension and muscular
CC dystrophy. The present sequence represents the DNA encoding the
CC NTAP1 fusion protein of the invention.
XX
XX Sequence 1582 BP; 464 A; 333 C; 329 G; 456 T; 0 other;
Query Match 77.8%; Score 1187; DB 24; Length 1582;
Best Local Similarity 99.6%; Pred. No. 2.3e-288;
Matches 1190; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 AGACCATGGAAGACCCCTCAAGCGACGCGCTCAAAAACCGCACACGATCATCAGACC 63
DB |||||||
DB 385 AGGAATGGAAGACCCCTCAAGCGACGCGCTCAAAAACCGCACACGATCATCAGACC 444
QY 64 AGACCATCGGACTTTTAATAAATTAATCTCAAAATTTAGCGGAATTTGCTTTTCTTGT 123
DB |||||||
DB 445 AAGACCATCGGACTTTTAATAAATTAATCTCAAAATTTAGCGGAATTTGCTTTTCTTGT 504
QY 124 ATAGACAATAGCTCATCAAAAGTAATCTACTAACAATTTTTTTAGTCTCTTTCTATTG 183
DB |||||||
DB 505 ATAGACAATAGCTCATCAAAAGTAATCTACTAACAATTTTTTTAGTCTCTTTCTATTG 564
QY 184 CCACATGCTTTCCGCACTTTGAGTTAGTACTAAAGCCGATFACCCATGACGAGATTTAG 243
DB |||||||
DB 565 CCACATGCTTTCCGCACTTTGAGTTAGTACTAAAGCCGATFACCCATGACGAGATTTAG 624
QY 244 AAGGTTTAACTTTAATTTGACCGAATCCAGAGCCCAATTCACGAGGTTTTCAAG 303
DB |||||||
DB 625 AAGGTTTAACTTTAATTTGACCGAATCCAGAGCCCAATTCACGAGGTTTTCAAG 684
QY 304 AGTTCTGACGACTTTGAATCAACTGATTTCTCAATTCGAATTAACACTGGTAACGGTT 363
DB |||||||
DB 685 AGTTCTGACGACTTTGAATCAACTGATTTCTCAATTCGAATTAACACTGGTAACGGTT 744
QY 364 TATTTTCTGAGAGGTTTAAATTTGGTTGACAAATTCCTAGAGACGTCAGAAACTAT 423
DB |||||||
DB 745 TATTTTCTGAGAGGTTTAAATTTGGTTGACAAATTCCTAGAGACGTCAGAAACTAT 804
QY 424 ATCATAGTAGGCTTTACCGTTAATTTGGTGATAGTACGAGGCTTAAAGCAATTA 483
DB |||||||

Db 805 ATCATAGTAGGCTTTTACCGTTAATTTGGTGATAGTACGAGAGCTTAAAGCAATTA 864
QY 484 ATGATTATGTTGAGAAAGCCACCGAGGTAAAGATCGTTGACCTAGTTAAAGAAATAGATC 543
DB |||||||
DB 865 ATGATTATGTTGAGAAAGCCACCGAGGTAAAGATCGTTGACCTAGTTAAAGAAATAGATC 924
QY 544 GTGATACCGCTTCCGCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAAGCTCCTT 603
DB |||||||
DB 925 GTGATACCGCTTCCGCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAAGCTCCTT 984
QY 604 TCGAGGTTAAAGATACCTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAG 663
DB |||||||
DB 985 TCGAGGTTAAAGATACCTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAG 1044
QY 664 TTCCAATGATGAAAGACTGGGTATGTTCAATATTCAACATTTGCAAAAAAATAAGTCTT 723
DB |||||||
DB 1045 TTCCAATGATGAAAGACTGGGTATGTTCAATATTCAACATTTGCAAAAAAATAAGTCTT 1104
QY 724 GGGTCTTAATGAAGATATTAGTAAAGCTACTGCTATTTTTTTTTTACCAGACGAAG 783
DB |||||||
DB 1105 GGGTCTTAATGAAGATATTAGTAAAGCTACTGCTATTTTTTTTTTACCAGACGAAG 1164
QY 784 GTAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATATTACTAAATTTTAGAGA 843
DB |||||||
DB 1165 GTAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATATTACTAAATTTTAGAGA 1224
QY 844 ACAGAGATCGTACGAGCGTCTCTGCACCTGCCAAAGTTAAGTATCACCAGTACTTACG 903
DB |||||||
DB 1225 ACAGAGATCGTACGAGCGTCTCTGCACCTGCCAAAGTTAAGTATCACCAGTACTTACG 1284
QY 904 ACTTAAATCTGTTTAGGCCAGTTAGGTATTACCAAGTTTTTTTCTAACGGTGCCGATT 963
DB |||||||
DB 1285 ACTTAAATCTGTTTAGGCCAGTTAGGTATTACCAAGTTTTTTTCTAACGGTGCCGATT 1344
QY 964 TGAGTGGTCTTACTGAAGAAGCTCCATTAAATTTAGTAAAGCTGTTCAAAAGCCGCT 1023
DB |||||||
DB 1345 TGAGTGGTCTTACTGAAGAAGCTCCATTAAATTTAGTAAAGCTGTTCAAAAGCCGCT 1404
QY 1024 TAACTATGATGAAAGGTACCGAGCGCGCGCGCTATGTTCTGGAGATATTCACAA 1083
DB |||||||
DB 1405 TAACTATGATGAAAGGTACCGAGCGCGCGCGCTATGTTCTGGAGATATTCACAA 1464
QY 1084 TGAGCATTCACAGAGGTTAAATTTAAATTAACCATTCCTTTCTGATGATCGAGCAGA 1143
DB |||||||
DB 1465 TGAGCATTCACAGAGGTTAAATTTAAATTAACCATTCCTTTCTGATGATCGAGCAGA 1524
QY 1144 ACACTAAAAGCCCATTTGTTTATGGGTAAGGTTGTCACCCCAACTCAGAAAGTGC 1198
DB |||||||
DB 1525 ACACTAAAAGCCCATTTGTTTATGGGTAAGGTTGTCACCCCAACTCAGAAAGTGC 1579

RESULT 7

ABK88015

ID ABK88015 standard; DNA; 1182 BP.

XX

AC ABK88015;

XX

DT 07-OCT-2002 (first entry)

XX

DE DNA encoding human alpha-1-antitrypsin (AAT) protein.

XX

XX Alpha-1-antitrypsin; AAT; human; gene; ds; protease inhibitor; malaria;
KW emphysema; asthma; chronic obstructive pulmonary disease; eczema;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1182

ID AAQ89254 standard; cDNA; 1312 BP.
 XX
 AC AAQ89254;
 XX
 DT 18-OCT-1995 (first entry)
 XX
 DE Human alpha-1-tryptsin cDNA.
 XX
 KW Alpha-1-tryptsin; protease-inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 28..1258
 FT FT *tag= a
 FT sig_peptide 28..99
 FT FT *tag= b
 FT mat_peptide 100..1255
 FT FT *tag= c
 XX
 XX US5399684-A.
 PN
 XX
 PD 21-MAR-1995.
 XX
 PF 20-MAY-1982; 82US-0380310.
 XX
 PR 20-MAY-1982; 82US-0380310.
 PR 07-FEB-1984; 84US-0638980.
 PR 03-MAR-1987; 87US-0022543.
 PR 15-DEC-1987; 87US-013190.
 PR 16-SEP-1988; 88US-0246912.
 PR 22-AUG-1989; 89US-0398288.
 PR 11-MAR-1991; 91US-0666450.
 PR 18-NOV-1992; 92US-0979556.
 PR 02-JUL-1993; 93US-0086442.
 XX
 PA (WASH-) WASHINGTON RES FOUND.
 XX
 PI Davie EW, Kurachi K, Thirumalachary C, Woo SLC;
 XX
 DR WPI: 1995-130740/17.
 DR P-PSDB; AAR71969.
 XX
 PT Human alpha-1-tryptsin (al-AT) cDNA sequence - can be used for
 PT the expression of al-AT
 XX
 PS Claim 1; Fig.1; 15pp; English.
 XX
 CC The sequence of a human alpha-1-antitrypsin cDNA clone is given in
 CC AAQ89254. Expression of the cDNA in host cell transformants has
 CC allowed production of recombinant alpha-1-antitrypsin.
 XX
 SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;
 Query Match 28.3%; Score 432.2; DB 16; Length 1312;
 Best Local Similarity 60.4%; Pred. No. 1.1e-98;
 Matches 713; Conservative 0; Mismatches 468; Indels 0; Gaps 0;
 QY 12 GAAGACCTCAAGGCGACCGCTCAAAACCGACACAGTCATCAGACCAAGACCAT 71
 DB 100 GAGGATCCCGAGGAGATCTGCCAGAGACAGATACATCCACCATGATCAGGATCAC 159
 QY 72 CGACATTTTAAATAAATTAATCCAAATTTAGCCGAATTTGCTTTTCTTTGATAGACAA 131
 DB 160 CCACCTTCAACAGATACACCCCACTTGGCTGAGTTGCGCTTCAGCGCTATACCGCCAG 219
 QY 132 TTAGCTCATCAAGTAATTTCTACTAATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 191
 DB 220 CTGGCACACCGATCCACAGACACCATATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 279
 QY 192 TTGCGCATCTTGATTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA 251
 DB 280 TTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGGATGAAATCTTGAGGCGCTG 339

QY 252 AACTTTAATTTGACCGAAATCCCAAGAGCCCAATTCACGAGGGTTTTCAGAGATTGTTG 311
 DB 340 AATTTCAACCTTCAGGAGATTCCGGAGGCTCAGATCCATGAGGCTTCCAGGAACTCCTC 399
 QY 312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAATCTACTGTAACGGTTTATTTTGG 371
 DB 400 CGTACCCCTCAACAGCCAGACAGCCAGCTCCAGCTGACCCAGCAATGGGCTTCTCCTC 459
 QY 372 TCTGAAGGTTTAAATTTGTTGACAAATTCCTAGAAGACGTCAGAAACTATATATCATAGT 431
 DB 460 AGCGAGGCGCTGAAGCTAGTAGTAAGTTTTCGAGGATGTTTAAAGTTCGTACCACTCA 519
 QY 432 GAGGCTTTTACCGTTAATTTTGGTGATCTAGGAGCTAAAGCAAGCAAAATTAATGATTAT 491
 DB 520 GAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAACACAGATCAACGATTAC 579
 QY 492 GTTGAGAAAGGCACCCAGGGTAAGATCTTGACCTAGTTTAAAGAAATAGATCGTGATACC 551
 DB 580 GTGAGAGGGTACTCAAGGGAATTTGTTGATTTGGTCAAGGAGCTTGACAGAGACACA 639
 QY 552 GTCCTTCGCATAGTTAACTATATTTTTCAGGGTAAAGTGGGAACGTCCTTTTCGAGGTT 611
 DB 640 GTTTTGTCTGTGGTGAATTAATCTCTTTTAAAGCAAAATGGAGAGACCCCTTTGAAGTC 699
 QY 612 AAAGATACTGAAGAGAGATTTTCATCTGTCATCAAGTTACTACTGTCAAAAGTTCCAATG 671
 DB 700 AAGGACACCGAGGAAGGAGCTTCCAGTGGACAGGTCACCCAGTTGGAAGGTCCTTAT 759
 QY 672 ATGAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAAATTTAAGTCTTCTGGGCTTA 731
 DB 760 ATGAAGCGTTTGGCATGTTTAACTCCAGCATTTGTAAAGAGCTGTCCAGCTGGGCTGTG 819
 QY 732 TTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTTTTACCAAGACGAGGTAAGCTT 791
 DB 820 CTGATGAAATACCTGGGCAATGCCACGCCCATCTTCTTCTGCTGATGAGGGGAACTA 879
 QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATTAATTAATTTTGTAGAGAACGAGAT 851
 DB 880 CAGCACCTGGGAAATGAACCTCACCACGATATCATCCAAAGTTCTCTGGGAAATGAAGAC 939
 QY 852 CGCTGAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 911
 DB 940 AGAAGGCTGCGCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAG 999
 QY 912 TCTGTTTATAGCCAGTTAGGTATTTACCAAGTTTTCCTAACGGTCCGATTTGAGTGGT 971
 DB 1000 AGCGTCTCTAGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGCTGACCTCTCGGG 1059
 QY 972 GTTACTGAAGAGCTCCCATTAATAATTTGAGTAAAGCTGTTCACAAAGCCGCTTAACTATT 1031
 DB 1060 GTCACAGAGGAGGACCCCTCCAAAGCTCTCCAAAGCCGTCGATAAGGCTGTGCTGACCATC 1119
 QY 1032 GATGAAAGGGTACCGAGCGCCGCGGCTATGTTCTCTGGAAGCTATTTCCAATGAGCAT 1091
 DB 1120 GACGAGAAAGGACTGAAGCTGCTGGGCGCATGTTTTTAGAGGCCATACCCATGCTCTATC 1179
 QY 1092 CCACAGAAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151
 DB 1180 CGCCCGAGGTCAGATTTCAACAAACCCCTTTGCTTCTTCTTAATGATTGAACAAATACCAAG 1239
 QY 1152 AGCCCATTTTATGGGTAAAGTTGTCAACCCCACTCAGAA 1192
 DB 1240 TCTCCCTCTTTCATGGGAAAGTGTGAATCCCAACCAAA 1280
 RESULT 10
 ID AAQ89254
 XX
 ID AAQ89254 standard; cDNA; 1312 BP.
 XX
 XX AAQ89254;
 XX
 DT 21-AUG-1998 (first entry)

XX OS Homo sapiens.
 XX PN US6025161-A.
 XX PD 15-FEB-2000.
 XX PF 20-JAN-1998; 98US-0009581.
 XX PR 07-JUN-1995; 95US-0479545.
 XX PR 20-MAY-1982; 82US-0380810.
 XX PR 07-FEB-1984; 84US-0638980.
 XX PR 03-MAR-1987; 87US-0022543.
 XX PR 15-DEC-1987; 87US-0133190.
 XX PR 16-SEP-1988; 88US-0246912.
 XX PR 22-AUG-1989; 89US-0398288.
 XX PR 11-MAR-1991; 91US-0666450.
 XX PR 18-NOV-1992; 92US-0979556.
 XX PR 02-JUL-1993; 93US-0086442.
 XX PA (WASH-) WASHINGTON RES FOUND.
 XX PI Woo SLC, Thirumalachary C, Kurachi K, Davie BW;
 XX DR WPI; 2000-181811/16.
 XX DR P-PSDB; AAY78890.
 XX PT Preparing alpha1-antitrypsin for inhibiting neutrophil elastase
 PT involves transfecting host cell with vector comprising
 PT alpha1-antitrypsin DNA sequence that hybridizes to human
 PT alpha1-antitrypsin cDNA, or its complement -
 XX PS Claim 1; Fig 1; 16pp; English.
 XX CC This sequence represents the human alpha1-antitrypsin nucleotide
 CC sequence. Alpha1-antitrypsin is an important protease inhibitor, the
 CC major function of which is to inhibit neutrophil elastase. Low levels of
 CC alpha1-antitrypsin in the blood are associated with chronic obstructive
 CC pulmonary emphysema and infantile liver cirrhosis. A vector comprising a
 CC mammalian alpha1-antitrypsin DNA sequence that hybridizes to human
 CC alpha1-antitrypsin cDNA can be introduced into a host cell in a method
 CC for the production of alpha1-antitrypsin.
 XX SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;
 Query Match 28.3%; Score 432.2; DB 21; Length 1312;
 Best Local Similarity 60.4%; Pred. No. 1.le-98;
 Matches 713; Conservative 0; Mismatches 468; Indels 0; Gaps 0;
 QY 12 GAAGACCTCAAGCGGCGGCTCAAAACCGACACAGTCATCAGGACCAAGACCAT 71
 DB 100 GAGGATCCCGGAGATGTCGCCAGACAGAGATACATCCACCATGATCAGGATCAC 159
 QY 72 CCGACTTTTAAATAATTAATCTCCAAATTTAGCCGAATTTGCTTTTGTATAGACAA 131
 DB 160 CCAACCTTCAACAAGATACCCCACTTGGCTGAGTTCGCTTACGCTATATACCCGAG 219
 QY 132 TTAGCTCATCAAGTAATTTACTATACATTTTTTTTAGTCTCTTATTTGCACTGCT 191
 DB 220 CTGGCACACCATGTCACACAGACCAATATCTTCTTCTCCCGAGTGAGCATCGTACAGCC 279
 QY 192 TTGGCCATGTTAGTTAGTACTAAGCGGATACCCATGACGAGATTTTAGAGGCTTTA 251
 DB 280 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACATCAGATGAAATCTGGAGGCGCTG 339
 QY 252 AACTTTTAAATTTGACCGAATCCAGAGGCCAAATTCAGAGGGTTTTCAAGAGTTGTG 311
 DB 340 AATTTCAACCTCAAGGATTTCCGAGGCTCAGATCCATGAAGGCTTCCAGGAACCTCCTC 399
 QY 312 AGAATTTGAATCAACTGATTTCTCAATTTGAATTTAACTGCTGGTAACGGTTATTTTGG 371
 DB 400 CGTACCTCAACGACGACAGACCCAGCTCCAGCTGACCAACCGGCAATGGCTGTTCCTC 459

QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTTCTAGAAGACGCTCAAGAAACTATATCATAGT 431
 DB 460 AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 519
 QY 432 GAGGCTTTTACCGTTAAATTTTGGTGATCTGAGGAGCTTAAAAAGCAATTAATCATATAT 491
 DB 520 GAAGCCTTCACTGTCAACTTCGGGGACACCCGAGAGGCCCAAGAACAGATCAACCATATAC 579
 QY 492 GTTGAGAAAGGCCACCCAGGCTAAGATCGTTGACCTAGTTAAAGAAATTAAGATCGTATACC 551
 DB 580 GTGGAGAAGGGTACTCAAGGGAAATTTGGGATTTGGTCAAGGAGCTTGACAGACACACA 639
 QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGGTGAAGTGGGAACGCTTTCAGAGTT 611
 DB 640 GTTTTGGCTCTGGTGAATTTACATCTCTTTTAAAGGCAATGGGAGAGACCCCTTTGAAGTC 699
 QY 612 AAAGATACCTGAAGAGGAGATTTTTCATGTTGATCAAGTTTACTACTGTCAAAGTTTCCAATG 671
 DB 700 AAGGACACCGAGGAGAGGACTTCCACGCTGGACAGGCTGACCCACCGTGAAGGTGCTATG 759
 QY 672 ATGAAAGACTGGGTATGTTCAATATTCACATTCGAAAAAATTAAGTTCTTTGGGTCTTTA 731
 DB 760 ATGAAGCGTTTAGGCATGTTTAAACATCCAGCATTTGAAGAAGCTGTCCAGCTGGGTGCTG 819
 QY 732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTTTTACCAGAGCAAGGTAAAGCTT 791
 DB 820 CTGATGAATATCTGGGCAATGCCACCGCATCTTCTTCTGCTGATGAGGGGAAACTA 879
 QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATTTACTTAATTTTATAGAACACGAGAT 851
 DB 880 CAGCACCCTGGAATGAAGTCAACCCAGCATATCATCACCAGTTCTCTGGAANAATGAAGAC 939
 QY 852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACGGTACTTACGACTTAAAA 911
 DB 940 AGAAGGTCTGCCAGCTTACATTTACCAAACTGTCCATTTACTTGAACCTATGATCTGAAG 999
 QY 912 TCTGTTTTAGGCCAGTATGAGTATTTACCAAGTTTTTTTCTAACGGTGGCGATTTGAGTGGT 971
 DB 1000 AGCGTCTAGGTCAACTGGGCATCACTAAGGTCTTTCAGCAATGGGGCTGTCTCCGGG 1059
 QY 972 GTTACTTGAAGAAGCTTCCATTTAAATTTAGTAAAGCTGTTCACAAAGCCGCTCTTAATCTAT 1031
 DB 1060 GTCACAGAGGAGCCACCTGAAAGCTCTCCAGGCGGTGCATAGGCTGTGCTGACCATC 1119
 QY 1032 GATGAAAGGGTACCGAGGCCCGCGGCTATGTTCTTGGAAAGTATTTCCAATAGACANT 1091
 DB 1120 GACGAGAAAGGACTGAAGCTGTGGGGCCATGTTTTTTAGAGGCCATACCCCATGCTATC 1179
 QY 1092 CCACGAGAGTTAAATTTAAATAAACCATTCGTTTTTCTTGATCATCGACAGACACTAAA 1151
 DB 1180 CGCCCGAGGCTCAAGTTTCAACAAACCCCTTTGCTTCTTAATGATTTGAACAAATACCAAG 1239
 QY 1152 AGCCCATTTTATGGGTAAGGTTGTCAACCCCACTCAGAA 1192
 DB 1240 TCTCCCTCTTCACTGGGAAAGTGGTGAATCCACCCCAAAA 1280
 RESULT 12
 AAS45052
 ID AAS45052 standard; cDNA; 1367 BP.
 XX AC AAS45052;
 XX XX
 XX DT 18-DEC-2001 (first entry)
 XX XX
 XX DE cDNA encoding novel human secretory protein, Seq ID No 133.
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;

severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
fertility; analgesic; pain; antigen; ss.

Homo sapiens.

WO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-0504942.

07-MAR-2000; 2000US-0519705.

19-MAY-2000; 2000US-0574454.

17-JUN-2000; 2000US-0596193.

14-JUL-2000; 2000US-0616847.

19-SEP-2000; 2000US-0665363.

20-OCT-2000; 2000US-0693267.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

Zhao QA, Yang Y, Driemanac RT, Zhang J, Chen R, Xue AJ, Wang J;

WPI; 2001-589934/66.

P-PSDB; AAU28152.

Novel polypeptides and nucleic acids obtained from cDNA libraries
prepared from various human tissues, for diagnosis and treatment of
cancer, neurological, inflammatory, and autoimmune disorders -

Claim 1: SEQ ID No 133; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I)
and polynucleotides (II). (I) and (II) are useful for treating
inflammatory conditions such as arthritis, nephritis, Crohn's disease,
ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
involved in increasing haematopoiesis, stem cell survival, bone growth
and remodeling. (I), (II) and modulators of (I) are useful for
prophylaxis or treatment of one or more cancers. (II) is also useful for
creating transgenic animals useful for studying the in vivo activities of
the polypeptide as well as for studying modulators of the polypeptides.
(I) induces the proliferation of neural cells and regeneration of nerve
and brain tissue and is useful for the treatment of central and
peripheral nervous system diseases and neuropathies, such as Alzheimer's,
Parkinson's disease, Huntington's disease, and amyotrophic lateral
sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
activity, regulation of haematopoiesis and is useful for treating myeloid
or lymphoid cell disorders, platelet disorders such as thrombocytopenia
and for regeneration of bone, cartilage, tendon, ligament and/or nerve
tissue growth, and in tissue repair, healing of burns, incisions,
ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
disorders, or periodontal disease. Furthermore, (I) is also useful for
gut protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues, various immune deficiencies and
disorders including severe combined immunodeficiency (SCID), bacterial or
fungal infections, autoimmune disorders e.g. multiple sclerosis,
rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
reactions and conditions, such as asthma or other respiratory problems.
In addition, (I) affects biorhythms or circadian cycles of rhythms,
fertility, metabolism, catabolism, anabolism, storage or elimination of
dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
analgesic effects or other pain reducing effects, immunoglobulin like
activity and can act as an antigen in a vaccine composition to raise an
immune response. AAS44920-AAS45295 represent novel human secreted protein
coding sequences of the invention.

Sequence 1367 BP; 357 A; 392 C; 323 G; 295 T; 0 other;

Query Match 28.1%; Score 429.2; DB 22; Length 1367;

Best Local Similarity 60.7%; Pred. No. 6.6e-98;

Matches 718; Conservative 0; Mismatches 463; Indels 1; Gaps 1;

Qy 12 GAAGACCCCTCAAGCGGACGCCGCTCAAAAAACCGACACAGTATCATCAGCAGCAAGACCAT 71
Db 105 GAGGATCCCGAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGGATCAC 164
Qy 72 CCGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGCAA 131
Db 165 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTCGCCCTTACGCTTATACCGCAG 224
Qy 132 TTAGCTCATCAAAAGTAATTTCTACTAACAATTTTATTTAGTCTCTGTTTCTTATTTGCCACTGCT 191
Db 225 CTGGCACACAGTCCACAGCAGCAATATCTTCTTCCCGCAGTGAGCATCGCTACAGCC 284
Qy 192 TTGCCCATGTTGAGTTTAGTACTTAAAGCCGATACCCATGACGAGATTTTGAAGGTTTA 251
Db 285 TTTGCAATGCTCTCCCTGGGACCAAGGCTGACACTCAGATGAAATCTCTGGAGGCGCTG 344
Qy 252 AACTTTTAAATTTGACCGAAATCCCAAGAGCCCAATTTACGAGGGTTTTCAGAGTTGTTG 311
Db 345 AATTTCAACCTTCAGGAGATTCGGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCCTC 404
Qy 312 AGAATTTTGAATCAACCTGATTTCTCAATTTCAATTTACTTACTGTTACGGTATTTATTTTG 371
Db 405 CGTACCCTCAACAGCCAGACAGCCAGCTCCAGCTGACCCAGCAATGCGCTGTTCCTC 464
Qy 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGACAGCTCAAGAACTATATCATAGT 431
Db 465 AGCGAGGCGCTGAAGCTAGTGGATAGTTTTGGAGATGTTTAAAGTTTGTACCACTCA 524
Qy 432 GAGCGTTTACCGTTAAATTTTGGTGAT - ACTGAGGAAGCTTAAAAAGCAAAATTAATGATTA 490
Db 525 GAAGCTTCACTGTCAACTTCGGGGATCCGGAAGAGGCCAAGAACAGATCAACGATTA 584
Qy 491 TGTGTGAGAAAGGCCACCGAGGTAAGATCGTTGACCTAGTTTAAAGAAATTAGATCGTGATAC 550
Db 585 CGTGAGAAAGGTTACTCAAGGGAAAATTTGTGATTTTGTCAAGGAGCTTGACAGAGACAC 644
Qy 551 CGTCTTGCCTAGTTTAACTATATTTTTCAGGGTAAAGTGGAGAGCTCTTTCGAGGT 610
Db 645 AGTTTTTCTCTGTTGATTTACATCTTCTTTAAAGGCAAAATGGGAGAGAGCTTTTGAAGT 704
Qy 611 TAAAGATTAAGAGGAAAGATTTTCATTTGATCAAGTTTACTTCTCAAGTTTCAAGTTCAAT 670
Db 705 CAAGGACCCGAGGACGAGGACTTCCAGCTGGACCCAGCTGACCCAGCTGAAGCTCCCTAT 764
Qy 671 GATGAAAGACTGGGTATGTTTCAATATTCACATTCACAAATTAAGTTTCTTGGGTCTT 730
Db 765 GATGAAGCGTTTGGGATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTACT 824
Qy 731 ATTAATGAAGTATTTAGTACGCTACTGCTATTTTCTTTTACCGACGAGGTAAGCT 790
Db 825 GCTAATGAATACCTGGGCAATGCCCGCATCTTCTTCTCCTGATGAGGGGAAACT 884
Qy 791 TCAACATTTTAGAGAAATGAGTTGACTCATGACATTTACTATAATTTTAGAGAACGAGGA 850
Db 885 ACAGCCTGGAATGNACTCACCAGATATCATCACAAGTTCTCTGGAATGAAGA 944
Qy 851 TCCTGCTAGCGCTTCTCTGACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAA 910
Db 945 CAGAAGGTCTCCAGCTTACATTTACCCAACTGTCTCCATTTACTGGAACCTATGATCTGAA 1004
Qy 911 ATCTGTTTATGAGCCAGTTAGTATTTACCAAGTTTCTTCTAACGGTCCGATTTGAGTGG 970
Db 1005 GAGCGTCTCGGTCACTGGGCACTACTAAGGTTCTCAGCAATGGGCTGACCTCCGG 1064
Qy 971 TGTACTGAAGAAGCTCCATTTAAATTTAGTAAAGCTGTTTCAACAAAGCGCTTTAACTAT 1030
Db 1065 GGTACAGAGGAGGACCCCTGAGCTCTCAAGCCGCTGCATAAGGCTGTGCTGACCAT 1124
Qy 1031 TGATGAAAGGTTACCGAGGCGCGGCTATGTTTCTTGGAAGCTATTTCAATGAGCAT 1090
Db 1125 GCAGGAGAAGGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCCATACCAATGTCTAT 1184
Qy 1091 TCCACCAGAAAGTTAAATTTAATAAACCATTCGTTTTTCTGTATGATCGAGCAGACACTAA 1150

Db 1185 CCCCCAGAGGTCAAGTTCAACAAACCCCTTGTCTCTTATGATGACAAATACCAA 1244
QY 1151 AAGCCATTTTATGGTGAAGTGTCAACCAACTCAGAA 1192
Db 1245 GTCTCCCTCTTCATGGGAAAGTGGTGAATCCCAACCCAAAA 1286

RESULT 13

AAV41726

ID AAV41726 standard; DNA; 1185 BP.

XX AC

XX AAV41726;

XX DT 20-NOV-1998 (first entry)

XX DE

XX Native coding sequence of mature alpha1-antitrypsin (AAT).

XX Protein expression; monocotyledon plant cell;

KW glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;

KW ATRII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;

KW antithrombotic; blood replacement; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO9836085-A1.

XX PD

XX 20-AUG-1998.

XX PF

XX 13-FEB-1998; 98WO-US03068.

XX PR

XX 13-FEB-1997; 97US-0038170.

XX PR

XX 13-FEB-1997; 97US-0037991.

XX PR

XX 13-FEB-1997; 97US-0038168.

XX PR

XX 13-FEB-1997; 97US-0038169.

XX PA

XX (PHYT-) APPLIED PHYTOLOGICS INC.

XX PI

XX Rodriguez RL, Sutliff TD;

XX WPI; 1998-467179/40.

XX DR

XX P-PSDB; AAW59839.

XX PT

XX Expressing mature, glycosylated proteins in monocotyledonous plant

XX cells - from chimeric gene including signal peptide sequence,

XX specifically therapeutic agents and industrial enzymes

XX Disclosure; Page 29; 53pp; English.

XX The present sequence represents the native coding sequence of mature

XX alpha1-antitrypsin (AAT). The protein is used to exemplify the

XX invention. The specification describes a method for producing mature

XX heterologous protein in monocotyledonous plant cells. The method

XX comprises transforming the cells with a chimeric gene comprising a

XX monocotyledon transcription regulator, inducible either during seed

XX maturation or by adding/removing a small molecule, DNA encoding the

XX heterologous protein, and DNA encoding a signal peptide, with

XX the signal peptide causing secretion of the protein from the cell.

XX Proteins expressed in this manner include mature glycosylated alpha

XX 1-antitrypsin (AAT) with a glycosylation pattern that significantly

XX increases its serum half-life, mature glycosylated antithrombin III

XX (ATRII), mature human serum albumin (HSA) having the native folding

XX pattern as shown by bilirubin-binding characteristics, or mature active

XX subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for

XX treating emphysema, ATRII as antithrombotic and HSA as blood replacement)

XX or as industrial enzymes (BPN' is used in detergents).

XX SQ

XX Sequence 1185 BP; 328 A; 324 C; 283 G; 250 T; 0 other;

XX Query Match 28.1%; Score 429; DB 19; Length 1185;

XX Best Local Similarity 60.2%; Pred. NO. 7.1e-98;

XX Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCCCTCAAGCGCAGCCGCTCAAAAACCCGACACCCAGTCATCAGCACCAAGACCAT 71
Db 1 GAGATCCCAGGAGATGCTGCCAGAGAGATACATCCCACCATGATCAGGATCAC 60
QY 72 CCGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTTGTATAGACAA 131
Db 61 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTCGCTTTCAGCCTATATACGCCAG 120
QY 132 TTAGCTCATCAAAAGTAAATTTCTACTAATATTTTCTTTAGTCTCTCTTTCTATTGCGACTGCT 191
Db 121 CTGGCACACAGTCCCAACAGCACCAATATCTCTCTCCCAAGTGAGCATCGGTACAGCC 180
QY 192 TTGCCCATTGTTAGTCTTAAAGCCGATACCCATCAGCAGATTTTATAGAGGTTTA 251
Db 181 TTGCAATGCTCTCCCTGGGACCAAGGCTGACATCAGATGAATCTCTGGAGGCGCTG 240
QY 252 AACTTTTAAATTTGACCGAAATCCCAGAGGCCAAATTTACAGAGGTTTTCAGAGTTGTTG 311
Db 241 AATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACCTCTC 300
QY 312 AGAATTTGAAATCAACCTGATTTCTCAATTCGAATTAATTAATTAATTAATTAATTAAT 371
Db 301 CGTACCCTCAACCCAGCAGACAGCCAGCTCCAGCTGACCCAGGCAATGGCCTGTTCCCTC 360
QY 372 TCTGAAGGTTTAAATTTGTTGACAAATTTCTAGAAGACGCTCAAGAACTATATCATAGT 431
Db 361 AGCAGGCGCTGAAGCTAGTGGATAGTTTGTGGAGATGTTTAAAGTTGTACCACTCA 420
QY 432 GAGGCTTTTACCGTTAAATTTTGTGTGATCTGAGGAAGCTAAAAAGCAAAATTAATGATTAT 491
Db 421 GAACCTTCTACTGTCAACTTCGGGGACACGAGAGGCCCAAGAAACAGATCAACGATTAC 480
QY 492 GTTGAGAAAGCACCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAGATCTGATATACC 551
Db 481 GTGGAGAAGGGTACTCAAGGGAATTTGTGGATTTTGTGTCAGGAGCTTGACAGAGACACA 540
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGAGGTAAGTGGGAACGCTCTCTCGAGGTT 611
Db 541 GTTTTGTCTCTGGTGAATTTACATCTTCTTAAAGGCAATTTGGAGAGACCTTTGAAGTC 600
QY 612 AAAGATATCTGAAGAGGAGGATTTTTCATGTTGATCAAGTTACTACTGTCAAGATTTCCAATG 671
Db 601 AAGCACACCAGGAGGAGGAGGACTTCCAGCTGGACCCAGCTGACCCAGTGAAGGTGCTATG 660
QY 672 ATGAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAAAATTAAGTTCTTGGGCTTA 731
Db 661 ATGAAGGCTTTAGGCATGTTTAAACATCCAGCACTGTAAAGAGCTGTCCAGCTGGGTGCTG 720
QY 732 TTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTCAGAGGTAAGGTAAGCTT 791
Db 721 CTGATGAATACCTGGGCAATGCCCGCCATCTTCTCTGCTGATGAGGGGAACTA 780
QY 792 CAACATTTAGAGAATGAGTTGACTCATGACATTAATTAATTAATTTTAGAGAACGAGGAT 851
Db 781 CAGCACCTGGAATAATGAACCTCACCCAGATATCATCACCAGTTCCTGGAATAATGAAGAC 840
QY 852 CGTCTAGCGCTTCTCTGCACCTCCCAAGTTAAGTATCAACCGGTACTTACGACTTAAAA 911
Db 841 AGAAGGCTTGCACGCTTACATTTTACCACCAACTGTCCAACTATGGAACCTATGATCTGAAG 900
QY 912 TCTGTTTTAGGCCAGTTAGGTATTTTACCAAAAGTTTTCACCGTCCGCGATTTGAGTGGT 971
Db 901 AGCGTCTGGTCAACTGGGCACTCACTAAGGTCTTTACAGCAATGGGCTGACCTCTCCGGG 960
QY 972 GTTACTAGAGAAGCTCCATTAAAAATTTGAGTAAAGCTGTTCACAAAGCGGCTTTAACTATT 1031
Db 961 GTCACAGAGGAGGCAACCCCTGAAGCTCTCCAAAGGCGGTGCATAAGGCTGTGCTGACCATC 1020
QY 1032 CATGAAAGGTTACCGAGGCGCGCGCTATGTTCTCTGGAGCTATTTCCCAATCAGCATT 1091
Db 1021 GACGAGAAAGGACTGAAGCTGTGGGCGCCATGTTTTTAGAGGCCATACCATCTCTATC 1080
QY 1092 CCACCAGAAGTTAAATTTAATTAACCACTTCTGTTTTTCTGATGATCGAGCAGAACACTAAA 1151

Db 1081 CCCCCGAGGTCAAGTTCACCAACCCCTTGTCTTCTTAATGATTGAACAAATACCAAG 1140
QY 1152 AGCCATTGTTTATGGTAAGTGTGTCACCCCAACTCAGAA 1192
Db 1141 TCTCCCTCTTTCATGGGAAAGTGGTGAATCCACCCAAA 1181

RESULT 14
AAQ31403
ID AAQ31403 standard; DNA; 1352 BP.

XX AAQ31403;
AC AAQ31403;
XX
XX 23-MAR-1993 (first entry)
DT
XX Human alpha-1 antitrypsin.
DE
XX Plasmid; pcMW4; liposome; antiprotease; lung; emphysema;
KW adult respiratory distress syndrome; ARDS; ss.
XX Homo sapiens.
OS
XX W09219730-A.
PN
XX 12-NOV-1992.
PD
XX 27-MAR-1992; 92WO-US02465.
PF
XX 24-APR-1991; 91US-0690283.
PR
XX (UYVA-) UNIV VANDERBILT.
PA
XX Brigham K, Canonico A, Conary J, Meyrick B;
PI WPI; 1992-398857/48.
XX
XX Human alpha-1 anti-trypsin contg. plasmid - for treatment of
PT anti-protease deficiency in emphysema and other lung diseases
PT
XX Disclosure; Fig 6a-6b; 32pp; English.
PS
XX A plasmid consisting of a pcMW4 expression vector including a coding
CC sequence of human alpha-1 antitrypsin may be incorporated into
CC liposomes capable of targeting specific tissue. The plasmid is then
CC capable of expression of the gene extrachromosomally in the cells of
CC the target tissue and is unincorporable into the chromosome of the
CC cells of the target tissue. Thus, the liposome including the
CC plasmid can be used in a method for treating a deficiency of the
CC gene product in cells of the target tissue.
CC The specific use of the human alpha-1 antitrypsin is significant as
CC this antiprotease is important in protecting the lungs against
CC emphysema. The adult respiratory distress syndrome (ARDS) is thought
CC to involve a relative deficiency of antiprotease activity.
CC Therefore, the delivery of a functioning alpha-1 antiprotease
CC gene to the lungs can be therapeutic in many human conditions
CC characterised by injury of the lungs.
XX
XX Sequence 1352 BP; 349 A; 386 C; 325 G; 292 T; 0 other;

Query Match 28.18; Score 429; DB 13; Length 1352;
Best Local Similarity 60.28; Pred. No. 7.4e-98;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGAGCGCGCTCAAAAAACCGACACAGTCATCAGCAACCAAGACCAT 71
Db 92 GAGGATCCCCAGGAGATGCTGCCAGAGACAGATACATCCCATGATCAGAGATCAC 151
QY 72 CGACTTTTAAATAAATTACTCAAAATTTAGCCGAATTTGCTTTTCTTTGATPAGACAA 131
Db 152 CCAACCTTCAACAGATCACCCCAACCTGCTGAGTTCGCTTCAGCCCTATACCGCCAG 211
QY 132 TTAGCTCATCAAGTAATTTCTACTAACATTTTTTTTAGTCTCTGTTTCTATGCCCAC 191

RESULT 15

ABL67511
ID ABL67511 standard; DNA; 1352 BP.
XX
AC ABL67511;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5848.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
XX WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233167P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236039P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
DR
XX
PT Screening for anti-neoplastic agent involves exposing cells to a

PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX Claim 1; SEQ ID 5848; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 1352 BP; 349 A; 386 C; 325 G; 292 T; 0 other;
Query Match 28.1%; Score 429; DB 24; Length 1352;
Best Local Similarity 60.2%; Pred. No. 7.4e-98;
Matches 71; Conservative 0; Mismatches 470; Indels 0; Gaps 0;
QY 12 GAAGACCCTCAAGCGGACGCGCTCAAAAACCGACACAGATCATCCAGCAAGACCAT 71
DB 92 GAGGATCCCAGGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGATCAC 151
QY 72 CCGACTTTTAAATAATTTACTTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131
DB 152 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTCGCTTTCAGCTATATACGCCAG 211
QY 132 TTAGCTCATCAAGTAATTTACTTAACATTTTTTTAGTCTCTTTCTATGCCACTGCT 191
DB 212 CTGGCACACAGTCCACAGACCAATATCTTCTCTCCAGTGAGGATGCTGCTACAGCC 271
QY 192 TTCGCATTTGAGTTTATAGTTACTAAAGCCGATACCCATGACGAGATTTTAAAGAGTTTA 251
DB 272 TTTGCAATGCTCTCCCTGGGACCAAGGCTCACACTCAGATGAATCTCTGGAGGCGTG 331
QY 252 AACTTTAATTTGACCGAATCCAGAGCCCAATTTACGAGGGTTTTCAGAGTTGTTG 311
DB 332 AATTTCAACCTCAGGAGATTTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAATCTCTC 391
QY 312 AGAAGCTTTGAATCAACCTGATTTCAATTTGCAATTTAACTACTGTAACGGTTTATTTTGG 371
DB 392 CGTACCTCAACAGCCAGACAGCGAGTCCAGCTGACCCAGCGCATGGCTGTCTCTC 451
QY 372 TCTGAAGTTTAAATTTGTTGACAAATTTCTAGAAGACGTCAGAAACATATATCATAGT 431
DB 452 AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 511
QY 432 GAGGCTTTTACGGTTAATTTTGGTGATCTAGGAGAGCTTAAAGCAAAATTAAGTATAT 491
DB 512 GAAAGCCTTCACTGTCAACTTCGGGAGACCCGAGAGGCGCAAGAACAGATCAAGCATTTAC 571
QY 492 GTTGAGAAAGGACCCAGGGTAAGATCGTTGACCTAGTTTAAAGAAATTAAGTCTGGTATACC 551
DB 572 GTGGAGAAGGGTACTCAAGGGAAATTTGATTTGGTCAAGGAGCTTGCACAGAGACACA 631
QY 552 GTCTTCGCACACTAGTTTAACTATATTTTTTCAAGGGTAAGTGGGACGCTCTCTTCAGGTT 611
DB 632 GTTTTTTGTCTGGTGAATTTACATCTCTTTTAAAGCAAAATGGAGAGACCCCTTTTGAAGTC 691
QY 612 AAAGTACTGAAGAGGAAGATTTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
DB 692 AAGGACACCGAAGAGGAGACTTCCACGTGGACCCAGGTGACCACCGTGAAGGTGCTGCTATG 751

